

DKGR-SEQS.ST25.txt

<210> 3

<211> 843

<212> DNA

<213> Corynebacterium species

<220>

<221> misc_feature

<223> "n" positions at both ends of sequence represent restriction endonuclease recognition sites; "n" positions at residues 49-51, and 55-57 represent areas of disagreement in the published sequence for wild type DKGR-B between Sonoyama and Powers, however, both published sequences encode the same amino acid

<400> 3

```
nnnatgccga acatccccac catcagcctc aacgacggac gccccttcnn ngagnnnggg      60
ctcggcacgt acaacctgcg cggcgacgag ggggtcgcgg ccatggtcgc cgcgatcgac      120
tcgggctacc gcctgctcga cacggcggtg aactacgaga acgagagcga ggtcggccga      180
gcggtgcgcg cgagcagcgt cgatcgcgac gagctcatcg tggcgagcaa gatcccgggc      240
cgccagcacg ggcgcgccga ggcggtcgac agcatccgcg gatcgctcga ccggctgggg      300
ctcgacgtga tcgacctgca gctgatccac tggccgaacc ccagcgtggg ccggtggctc      360
gacacctggc gcggcatgat cgacgcgcgc gaggcggggc tggtcgctc gatcggcgctc      420
tcgaacttca ccgagccgat gctgaagacc ctcatcgacg agaccggggg cacaccgcg      480
gtcaaccagg tcgagctcca cccgtacttc ccccaggcgg cgctgcgcgc gttccacgac      540
gagcacggca tccgcaccga gagctggagc ccgctcgccc ggcgcagcga gctgctcacc      600
gagcagctgc tgcaggagct ggcggtcgtc tacggagtga cgccgacgca ggtggtgctg      660
cggtggcacg tgcagctcgg cagcaccccg atccccaagt ccgccgaccc cgatcgccag      720
cgcgagaacg ccgatgtgtt cggttcgcc ctcaccgccg accaggtcga tgcgatctcg      780
ggcctcgagc gcgggcggct ctgggacggc gaccccgaca cgcacgaaga gatgtaghhh      840
nnn                                                                    843
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<210> 4

<211> 843

<212> DNA

<213> Corynebacterium species

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<400> 4
catatgccga acatcccgac catctctctg aacgacggtc gtccggtccc ggaactgggt    60
ctgggtacct acaacctgcg tggtagacgaa ggtgttgctg ctatggttgc tgctatcgac    120
tctggttacc gtctgctgga caccgctgtt aactacgaaa acgaatctga agttggtcgt    180
gctgttcctg cttcttctgt tgaccgtgac gaactgatcg ttgcttctaa aatccccgggt    240
cgtcagcacg gtcgtgctga agctgttgac tctatccgtg gttctctgga cgtctgggt    300
ctggacgtta tcgacctgca gctgatccac tggccgaacc cgtctgttgg tcgttggtg    360
gacacctggc gtggtatgat cgacgctcgt gaagctggtc tggttcgttc tatcgggtgc    420
tctaacttca ccgaaccgat gctgaaaacc ctgatcgacg aaaccggtgt taccctggct    480
gttaaccagg ttgaactgca cccgtacttc ccgcaggctg ctctgcgtgc tttccacgac    540
gaacacggta tccgtaccga atcttgggtc ccgctggctc gtcgttctga actgctgacc    600
gaacagctgc tgcaggaact ggctgttgtt tacggtgtta ccccgaccca ggttgttctg    660
cgttggcacg ttcagctggg ttctaccccg atcccgaaat ctgctgaccc ggaccgtcag    720
cgtgaaaacg cagacgtttt cggtttcgct ctgaccgctg accaggttga cgctatctct    780
ggtctggaac gtggtcgtct gtgggacggt gacccggaca cccacgaaga aatgtagaag    840
ctt                                                                    843

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<210> 5

<211> 277

<212> PRT

<213> Corynebacterium species

<400> 5

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Met Thr Val Pro Ser Ile Val Leu Asn Asp Gly Asn Ser Ile Pro Gln
1          5          10          15
Leu Gly Tyr Gly Val Phe Lys Val Pro Pro Ala Asp Thr Gln Arg Ala
20          25          30
Val Glu Glu Ala Leu Glu Val Gly Tyr Arg His Ile Asp Thr Ala Ala
35          40          45
Ile Tyr Gly Asn Glu Glu Gly Val Gly Ala Ala Ile Ala Ala Ser Gly
50          55          60
Ile Ala Arg Asp Asp Leu Phe Ile Thr Thr Lys Leu Trp Asn Asp Arg
65          70          75          80
His Asp Gly Asp Glu Pro Ala Ala Ala Ile Ala Glu Ser Leu Ala Lys
85          90          95

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Leu Ala Leu Asp Gln Val Asp Leu Tyr Leu Val His Trp Pro Thr Pro
 100 105 110
 Ala Ala Asp Asn Tyr Val His Ala Trp Glu Lys Met Ile Glu Leu Arg
 115 120 125
 Ala Ala Gly Leu Thr Arg Ser Ile Gly Val Ser Asn His Leu Val Pro
 130 135 140
 His Leu Glu Arg Ile Val Ala Ala Thr Gly Val Val Pro Ala Val Asn
 145 150 155 160
 Gln Glu Leu His Pro Ala Tyr Gln Gln Arg Glu Ile Thr Asp Trp Ala
 165 170 175
 Ala Ala His Asp Val Lys Ile Glu Ser Trp Gly Pro Leu Gly Gln Gly
 180 185 190
 Lys Tyr Asp Leu Phe Gly Ala Glu Pro Val Thr Ala Ala Ala Ala
 195 200 205
 His Gly Lys Thr Pro Ala Gln Ala Val Leu Arg Trp His Leu Gln Lys
 210 215 220
 Gly Phe Val Val Phe Pro Lys Ser Val Arg Arg Glu Arg Leu Glu Glu
 225 230 235 240
 Asn Leu Asp Val Phe Asp Phe Asp Leu Thr Asp Thr Glu Ile Ala Ala
 245 250 255
 Ile Asp Ala Met Asp Pro Gly Asp Gly Ser Gly Arg Val Ser Ala His
 260 265 270
 Pro Asp Glu Val Asp
 275

<210> 6

<211> 277

<212> PRT

<213> Corynebacterium species

<400> 6

Met Pro Asn Ile Pro Thr Ile Ser Leu Asn Asp Gly Arg Pro Phe Pro
 1 5 10 15
 Glu Leu Gly Leu Gly Thr Tyr Asn Leu Arg Gly Asp Glu Gly Val Ala
 20 25 30
 Ala Met Val Ala Ala Ile Asp Ser Gly Tyr Arg Leu Leu Asp Thr Ala
 35 40 45
 Val Asn Tyr Glu Asn Glu Ser Glu Val Gly Arg Ala Val Arg Ala Ser
 50 55 60
 Ser Val Asp Arg Asp Glu Leu Ile Val Ala Ser Lys Ile Pro Gly Arg
 65 70 75 80

DKGR-SEQS.ST25.txt

Gln His Gly Arg Ala Glu Ala Val Asp Ser Ile Arg Gly Ser Leu Asp
85 90 95

Arg Leu Gly Leu Asp Val Ile Asp Leu Gln Leu Ile His Trp Pro Asn
100 105 110

Pro Ser Val Gly Arg Trp Leu Asp Thr Trp Arg Gly Met Ile Asp Ala
115 120 125

Arg Glu Ala Gly Leu Val Arg Ser Ile Gly Val Ser Asn Phe Thr Glu
130 135 140

Pro Met Leu Lys Thr Leu Ile Asp Glu Thr Gly Val Thr Pro Ala Val
145 150 155 160

Asn Gln Val Glu Leu His Pro Tyr Phe Pro Gln Ala Ala Leu Arg Ala
165 170 175

Phe His Asp Glu His Gly Ile Arg Thr Glu Ser Trp Ser Pro Leu Ala
180 185 190

Arg Arg Ser Glu Leu Leu Thr Glu Gln Leu Leu Gln Glu Leu Ala Val
195 200 205

Val Tyr Gly Val Thr Pro Thr Gln Val Val Leu Arg Trp His Val Gln
210 215 220

Leu Gly Ser Thr Pro Ile Pro Lys Ser Ala Asp Pro Asp Arg Gln Arg
225 230 235 240

Glu Asn Ala Asp Val Phe Gly Phe Ala Leu Thr Ala Asp Gln Val Asp
245 250 255

Ala Ile Ser Gly Leu Glu Arg Gly Arg Leu Trp Asp Gly Asp Pro Asp
260 265 270

Thr His Glu Glu Met
275